

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,817

DATE: 05/08/2001
TIME: 11:50:03

Input Set : A:\ES.txt
Output Set: N:\CRF3\05082001\I674817.raw

ENTERED

3 <110> APPLICANT: Lorz, et al.
5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT AND
6 WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
8 <130> FILE REFERENCE: 514413-3849
10 <140> CURRENT APPLICATION NUMBER: 09/674,817
C--> 11 <141> CURRENT FILING DATE: 2001-04-06
13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03141
14 <151> PRIOR FILING DATE: 1999-05-07
16 <150> PRIOR APPLICATION NUMBER: 19820608.9
17 <151> PRIOR FILING DATE: 1998-05-08
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2997
25 <212> TYPE: DNA
26 <213> ORGANISM: Triticum aestivum L. cv. Florida
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30 <222> LOCATION: (3)..(296)
31 <223> OTHER INFORMATION: exon 1
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35 <221> NAME/KEY: CDS
36 <222> LOCATION: (2145)..(2921)
37 <223> OTHER INFORMATION: exon 3
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42 <222> LOCATION: (297)..(396)
43 <223> OTHER INFORMATION: intron 1
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48 <222> LOCATION: (397)..(1617)
49 <223> OTHER INFORMATION: exon 2
52 <220> FEATURE:
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54 <222> LOCATION: (1618)..(2144)
55 <223> OTHER INFORMATION: intron 2
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60 Ser Gly Pro Ala Pro Arg Leu Arg Arg Trp Arg Pro Asn Ala Thr
61 1 5 10 15
63 gcg ggg aag ggg gtc gcc gag gtg tgc gcc gcg gtt gtc gag gcg gcg 95
64 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala
65 20 25 30
67 acg aag gta gag gac gag ggg gag gag gac gag ccg gtg gcg gag gac 143
68 Thr Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp
69 35 40 45
71 agg tac gcg ctc ggc gcc gcg tgc agg gtg ctc gcc gga atg ccc gcg 191

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72 Arg Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala
73      50      55      60
75 ccg ctg ggc gcc acc gcg ctc gcc ggc ggg gtc aat ttc gcc gtc tat      239
76 Pro Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr
77      65      70      75
79 tcc ggc gga gcc acc gcc gcg gcg ctc tgc ctc ttc acg cca gaa gat      287
80 Ser Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp
81 80      85      90      95
83 ctc aag gcg gtgggggtgc ctcccgagta gagttcatca gctttgcgtg      336
84 Leu Lys Ala
87 cgccgcgcgc cccttttttg ggcctgcaat ttaagttttg tactggggca aatgctgcag      396
89 gat agg gtg acc gag gag gtt ccc ctt gac ccc ctg atg aat cgg acc      444
90 Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr
91      100      105      110
93 ggg aac gtg tgg cat gtc ttc atc gaa ggc gag ctg cac aac atg ctt      492
94 Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn Met Leu
95 115      120      125      130
97 tac ggg tac agg ttc gac ggc acc ttt gct cct cac tgc ggg cac tac      540
98 Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr
99      135      140      145
101 ctt gat gtt tcc aat gtc gtg gtg gat cct tat gct aag gca gtg ata      588
102 Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile
103      150      155      160
105 agc cga ggg gag tat ggt gtt cca gcg cgt ggt aac aat tgc tgg cct      636
106 Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro
107      165      170      175
109 cag atg gct ggc atg atc cct ctt cca tat agc acg ttt gat tgg gaa      684
110 Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu
111      180      185      190
113 ggc gac cta cct cta aga tat cct caa aag gac ctg gta ata tat gag      732
114 Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu
115 195      200      205      210
117 atg cac ttg cgt gga ttc acg aag cat gat tca agc aat gta gaa cat      780
118 Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His
119      215      220      225
121 ccg ggt act ttc att gga gct gtg tgc aag ctt gac tat ttg aag gag      828
122 Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu
123      230      235      240
125 ctt gga gtt aat tgt att gaa tta atg ccc tgc cat gag ttc aac gag      876
126 Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe Asn Glu
127      245      250      255
129 ctg gag tac tca acc tct tct tcc aag atg aac ttt tgg gga tat tct      924
130 Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser
131      260      265      270
133 acc ata aac ttc ttt tca cca atg aca aga tac aca tca ggc ggg ata      972
134 Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile
135 275      280      285      290
137 aaa aac tgt ggg cgt gat gcc ata aat gag ttc aaa act ttt gta aga      1020
138 Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe Val Arg

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139		295		300		305	
141	gag gct cac	aaa cgg gga att	gag gtg atc ctg gat gtt	gtc ttc aac		1068	
142	Glu Ala His	Lys Arg Gly Ile	Glu Val Ile Leu Asp Val	Val Phe Asn			
143		310		315		320	
145	cat aca gct	gag ggt aat gag aat	ggt cca ata tta tca	ttt aag ggg		1116	
146	His Thr Ala	Glu Gly Asn Glu Asn	Gly Pro Ile Leu Ser	Phe Lys Gly			
147		325		330		335	
149	gtc gat aat	act aca tac tat	atg ctt gca ccc aag	gga gag ttt tat		1164	
150	Val Asp Asn	Thr Thr Tyr Tyr	Met Leu Ala Pro Lys	Gly Glu Phe Tyr			
151		340		345		350	
153	aac tat tct	ggc tgt ggg aat acc	ttc aac tgt aat cat	cct gtg gtt		1212	
154	Asn Tyr Ser	Gly Cys Gly Asn Thr	Phe Asn Cys Asn His	Pro Val Val			
155	355		360		365		370
157	cgt caa ttc	att gta gat tgt tta	aga tac tgg gtg acg	gaa atg cat		1260	
158	Arg Gln Phe	Ile Val Asp Cys Leu	Arg Tyr Trp Val Thr	Glu Met His			
159		375		380		385	
161	gtt gat ggt	ttt cgt ttt gat ctt	gca tcc ata atg acc	aga ggt tcc		1308	
162	Val Asp Gly	Phe Arg Phe Asp Leu	Ala Ser Ile Met Thr	Arg Gly Ser			
163		390		395		400	
165	agt ctg tgg	gat cca gtt aac gtg	tat gga gct cca ata	gaa ggt gac		1356	
166	Ser Leu Trp	Asp Pro Val Asn Val	Tyr Gly Ala Pro Ile	Glu Gly Asp			
167		405		410		415	
169	atg atc aca	aca ggg aca cct ctt	ggt act cca cca ctt	att gac atg		1404	
170	Met Ile Thr	Thr Gly Thr Pro Leu	Val Thr Pro Pro Leu	Ile Asp Met			
171		420		425		430	
173	atc agc aat	gac cca att ctt gga	ggc gtc aag ctc att	gct gaa gca		1452	
174	Ile Ser Asn	Asp Pro Ile Leu Gly	Gly Val Lys Leu Ile	Ala Glu Ala			
175	435		440		445		450
177	tgg gat gca	gga ggc ctc tat caa	gta ggt caa ttc cct	cac tgg aat		1500	
178	Trp Asp Ala	Gly Gly Leu Tyr Gln	Val Gly Gln Phe Pro	His Trp Asn			
179		455		460		465	
181	gtt tgg tct	gag tgg aat ggg aag	tac cgg gac att gtg	cgt caa ttc		1548	
182	Val Trp Ser	Glu Trp Asn Gly Lys	Tyr Arg Asp Ile Val	Arg Gln Phe			
183		470		475		480	
185	att aaa ggc	act gat gga ttt gct	ggt ggt ttt gcc gaa	tgt ctt tgt		1596	
186	Ile Lys Gly	Thr Asp Gly Phe Ala	Gly Gly Phe Ala Glu	Cys Leu Cys			
187		485		490		495	
189	gga agt cca	cac cta tac cag gta	agtgtgtg gcaatacttg	taaataagatt		1647	
190	Gly Ser Pro	His Leu Tyr Gln					
191		500		505			
193	gagtgaatgt	cacctggatt ttttatatat	accacatgat gatacacatc	taaataatata		1707	
195	acaatcatag	tgtatgcata tgcatttggc	taagaagtat tagtgataac	actagtgcata		1767	
197	tatataggtt	ttaacacca acttgccaat	gaaggaacat agggctttct	agttatctta		1827	
199	tttatttgtc	cggtgaataa tccactgaaa	aattccagcc atgtcatttt	ttaggggggg		1887	
201	agaagaaact	atattgatit gcccccctaa	aagaagccat ctcagaattc	ataggtaagt		1947	
203	tgcttttctg	taaagaaagg aaaacgactt	catactttct atcgggtgcta	acttagctcg		2007	
205	atgtatatatt	gtaagatgaa tgccaaattt	aatttgtcgg ataatttgat	ctgttattca		2067	
207	caaatttcta	tttggtttct ctagaaatca	aaccagtaac ttgttatttg	cactgcaact		2127	
209	tcttattgat	taatcag gca gga gga	agg aaa cct tgg cac	agt atc aac		2177	

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210		Ala Gly Gly Arg Lys Pro Trp His Ser Ile Asn	
211		510 515	
213	ttt gta tgt gca cat gat gga ttt aca ctg gct gat ttg gta aca tat	2225	
214	Phe Val Cys Ala His Asp Gly Phe Thr Leu Ala Asp Leu Val Thr Tyr		
215	520 525 530		
217	aat aag aag tac aat tta cca aat ggg gag aac aac aga gat gga gaa	2273	
218	Asn Lys Lys Tyr Asn Leu Pro Asn Gly Glu Asn Asn Arg Asp Gly Glu		
219	535 540 545		
221	aat cac aat ctt agc tgg aat tgt ggg gag gaa gga gaa ttc gca aga	2321	
222	Asn His Asn Leu Ser Trp Asn Cys Gly Glu Glu Gly Glu Phe Ala Arg		
223	550 555 560		
225	ttg tct gtc aaa aga ttg agg aag agg cag atg cgc aat ttc ttt gtt	2369	
226	Leu Ser Val Lys Arg Leu Arg Lys Arg Gln Met Arg Asn Phe Phe Val		
227	565 570 575 580		
229	tgt ctc atg gtt tct caa gga gtt cca atg ttc tac atg ggt gat gaa	2417	
230	Cys Leu Met Val Ser Gln Gly Val Pro Met Phe Tyr Met Gly Asp Glu		
231	585 590 595		
233	tat ggc cac aca aaa ggg ggc aac aac aat aca tac tgc cat gat tct	2465	
234	Tyr Gly His Thr Lys Gly Gly Asn Asn Thr Tyr Cys His Asp Ser		
235	600 605 610		
237	tat gtc aat tat ttt cgc tgg gat aaa aaa gaa caa tac tct gag ttg	2513	
238	Tyr Val Asn Tyr Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser Glu Leu		
239	615 620 625		
241	cac cga ttc tgc tgc ctc atg acc aaa ttc cgc aag gag tgc gag ggt	2561	
242	His Arg Phe Cys Cys Leu Met Thr Lys Phe Arg Lys Glu Cys Glu Gly		
243	630 635 640		
245	ctt ggc ctt gag gac ttt cca acg gcc aaa cgg ctg cag tgg cat ggt	2609	
246	Leu Gly Leu Glu Asp Phe Pro Thr Ala Lys Arg Leu Gln Trp His Gly		
247	645 650 655 660		
249	cat cag cct ggg aag cct gat tgg tct gag aat agc cga ttc gtt gcc	2657	
250	His Gln Pro Gly Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe Val Ala		
251	665 670 675		
253	ttt tcc atg aaa gat gaa aga cag ggc gag atc tat gtg gcc ttc aac	2705	
254	Phe Ser Met Lys Asp Glu Arg Gln Gly Glu Ile Tyr Val Ala Phe Asn		
255	680 685 690		
257	acc agc cac tta ccg gcc gtt gtt gag ctc cca gag cgc gca ggg cgc	2753	
258	Thr Ser His Leu Pro Ala Val Val Glu Leu Pro Glu Arg Ala Gly Arg		
259	695 700 705		
261	cgg tgg gaa ccg gtg gtg gac aca ggc aag cca gca cca tac gac ttc	2801	
262	Arg Trp Glu Pro Val Val Asp Thr Gly Lys Pro Ala Pro Tyr Asp Phe		
263	710 715 720		
265	ctc acc gac gac tta cct gat cgc gct ctc acc ata cac cag ttc tcg	2849	
266	Leu Thr Asp Asp Leu Pro Asp Arg Ala Leu Thr Ile His Gln Phe Ser		
267	725 730 735 740		
269	cat ttc ctc tac tcc aac ctc tac ccc atg ctc agc tac tca tcg gtc	2897	
270	His Phe Leu Tyr Ser Asn Leu Tyr Pro Met Leu Ser Tyr Ser Val		
271	745 750 755		
273	atc cta gta ttg cgc cct gat gtt tgagagacca atatatacag taaataatat	2951	
274	Ile Leu Val Leu Arg Pro Asp Val		

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280 <210> SEQ ID NO: 2
281 <211> LENGTH: 764
282 <212> TYPE: PRT
283 <213> ORGANISM: Triticum aestivum L. cv. Florida
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295 Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp Arg
296          35          40          45
299 Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala Pro
300          50          55          60
303 Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser
304 65          70          75          80
307 Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu
308          85          90          95
311 Lys Ala Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn
312          100         105         110
315 Arg Thr Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn
316          115         120         125
319 Met Leu Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly
320          130         135         140
323 His Tyr Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala
324 145         150         155         160
327 Val Ile Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys
328          165         170         175
331 Trp Pro Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp
332          180         185         190
335 Trp Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile
336          195         200         205
339 Tyr Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val
340          210         215         220
343 Glu His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu
344 225         230         235         240
347 Lys Glu Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe
348          245         250         255
351 Asn Glu Leu Glu Tyr Ser Thr Ser Ser Lys Met Asn Phe Trp Gly
352          260         265         270
355 Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly
356          275         280         285
359 Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe
360          290         295         300
363 Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val
364 305         310         315         320
367 Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe
368          325         330         335

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date